

SEQUENCE LISTING

<110> Thompson, Mark
Knuth, Mark
Cardineau, Guy

<120> Bacillus thuringiensis Toxins with Improved Activity

<130> MA-702D2

<150> US 09/222,594

<151> 1998-12-28

<150> US 08/904,278

<151> 1998-07-31

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 1425

<212> DNA

<213> Bacillus thuringiensis

<400> 1

```

atgattattg atagtaaaac gactttacct agacattcac ttattcatac aattaaatta      60
aattctaata agaaatatgg tcctgggtgat atgactaatg gaaatcaatt tattatttca      120
aaacaagaat gggctacgat tggagcatat attcagactg gattaggttt accagtaaatt      180
gaacaacaat taagaacaca tgtaattta agtcaggata tatcaatacc tagtgatttt      240
totcaattat atgatgttta ttgttctgat aaaacttcag cagaatgggtg gaataaaaaat      300
ttatatcctt taattattaa atctgctaata gatattgctt catatgggttt taaagttgct      360
ggtgatcctt ctattaagaa agatggatat tttaaaaaat tgcaagatga attagataat      420
attgttgata ataattccga tgatgatgca atagctaaag ctattaaaga ttttaaagcg      480
cgatgtggta ttttaattaa agaagctaaa caatatgaag aagctgcaaa aaatattgta      540
acatcttttag atcaattttt acatgggtgat cagaaaaaat tagaaggtgt tatcaatatt      600
caaaaacggt taaaagaagt tcaaacagct cttaatcaag cccatgggga aagtagtcca      660
gctcataaag agttattaga aaaagtaaaa aatttaaaaa caacattaga aaggactatt      720
aaagctgaac aagattttaga gaaaaaagta gaatatagtt ttctattagg accattgtta      780
ggatttggtg tttatgaaat tcttgaaaat actgctgttc agcatataaa aaatcaaatt      840
gatgagataa agaaacaatt agattctgct cagcatgatt tggatagaga tgttaaaatt      900
ataggaatgt taaatagtat taatacagat attgataatt tatatagtca aggacaagaa      960

```

gcaattaaag ttttccaaaa gttacaaggt atttgggcta ctattggagc tcaaatagaa 1020
 aatcttagaa caacgctggtt acaagaagtt caagattctg atgatgctga tgagatacaa 1080
 attgaacttg aggacgcttc tgatgcttgg ttagttgtgg ctcaagaagc tcgtgatttt 1140
 acactaaatg cttattcaac taatagtaga caaaattttac cgattaatgt tatatcagat 1200
 tcatgtaatt gttcaacaac aaatatgaca tcaaataaat acagtaatcc aacaacaaat 1260
 atgacatcaa atcaatatat gatttcacat gaatatacaa gtttaccaaa taattttatg 1320
 ttatcaagaa atagtaattt agaataataa tgcctgaaa ataattttat gatatatggg 1380
 tataataatt cggattggta taataattcg gattgggtata ataata 1425

<210> 2

<211> 475

<212> PRT

<213> Bacillus thuringiensis

<400> 2

Met Ile Ile Asp Ser Lys Thr Thr Leu Pro Arg His Ser Leu Ile His
1 5 10 15

Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly Pro Gly Asp Met Thr
20 25 30

Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu Trp Ala Thr Ile Gly
35 40 45

Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val Asn Glu Gln Gln Leu
50 55 60

Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
65 70 75 80

Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
85 90 95

Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
100 105 110

Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
115 120 125

Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
 130 135 140

Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
 145 150 155 160

Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
 165 170 175

Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
 180 185 190

Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
 195 200 205

Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
 210 215 220

Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
 225 230 235 240

Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
 245 250 255

Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
 260 265 270

Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
 275 280 285

Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys Ile Ile Gly Met Leu
 290 295 300

Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
 305 310 315 320

Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
 325 330 335

Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
 340 345 350

Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
 355 360 365

Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
 370 375 380

Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp
 385 390 395 400

Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
 405 410 415

Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr
 420 425 430

Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
 435 440 445

Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
 450 455 460

Asp Trp Tyr Asn Asn Ser Asp Trp Tyr Asn Asn
 465 470 475

<210> 3
 <211> 1428
 <212> DNA
 <213> Bacillus thuringiensis

<400> 3
 atggtcattg acagcaagac gactctacca cggcactcac tgattcacac aatcaagctg 60
 aactctaaca agaagtatgg tcctggcgat atgactaacg ggaaccagtt catcatatcc 120
 aagcaagaat gggccacgat tggcgcatatc attcagactg gactcggctt accagtgaat 180
 gagcaacagc tgagaaccca cgtaaacttt agtcaagaca tcagcatacc atctgacttt 240
 tctcaactct acgatgtgta ttgtttctgac aagactagtg cagaatgggtg gaacaagaat 300
 ctctatcctt tgatcatcaa gtctgccaat gacattgctt catatgggtt caaagttgct 360
 ggtgatcctt cgatcaagaa agatgggttac ttcaagaagc ttcaagatga actcgacaac 420
 attgttgaca acaactccga cgacgatgag atagccaaag ccatcaagga cttcaaagca 480
 agatgtggca ttctcatcaa ggaagccaag cagtatgaag aagctgccaa gaacattgta 540
 acatcattgg atcagtttct ccatggagac cagaagaagc tcgaggggtg catcaacatt 600

cagaaacgtc tgaagagagt tcaaacagct ctgaatcaag cccatgggga atccagtcca 660
 gctcaciaag agcttcttga gaaagtgaag aacttgaaga ccacacttga gaggaccatc 720
 aaagctgaac aagacttgga gaagaaagta gagtacagct ttctacttgg acccttggtta 780
 ggctttgttg tctacgagat tcttgagaac actgctgttc aacacatcaa gaatcaaate 840
 gatgagatca agaaacagtt ggattctgag caacatgact tggatcgaga tgtgaagatc 900
 attggaatgc tcaacagcat caacactgac attgacaact tgtatagtca aggacaagaa 960
 gcaatcaaag tctttcagaa gctacaaggg atatgggcca ctattggagc tcagatagag 1020
 aatcttcgca ccacgtccct tcaagaagtc caagactctg atgatgctga tgagatacag 1080
 attgaacttg aggacgcatc tgatgcatgg ttagttgttg ctcaagaagc tcgtgacttc 1140
 aactgaatg cctactcaac caacagtcga cagaatctcc cgatcaatgt gatctcagat 1200
 tcatgcaatt gctccaccac caacatgaca tccaatcagt acagcaatcc aacaaccaac 1260
 atgactagca atcagtagat gattagccat gaggatacca gcttgcccaa caacttcag 1320
 ttgtcaagga attcgaacct ggagtacaag tgcctgaga acaacttcat gatctactgg 1380
 tacaacaact ccgattggta caacaattcg gattggtaca acaattaa 1428

<210> 4
 <211> 475
 <212> PRT
 <213> *Bacillus thuringiensis*
 <400> 4

Met Val Ile Asp Ser Lys Thr Thr Leu Pro Arg His Ser Leu Ile His
 1 5 10 15

Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly Pro Gly Asp Met Thr
 20 25 30

Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu Trp Ala Thr Ile Gly
 35 40 45

Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val Asn Glu Gln Gln Leu
 50 55 60

Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
 65 70 75 80

Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
85 90 95

Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
100 105 110

Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
115 120 125

Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
130 135 140

Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
145 150 155 160

Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
165 170 175

Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
180 185 190

Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
195 200 205

Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
210 215 220

Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
225 230 235 240

Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
245 250 255

Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
260 265 270

Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
275 280 285

Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys Ile Ile Gly Met Leu
290 295 300

Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
 305 310 315 320

Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
 325 330 335

Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
 340 345 350

Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
 355 360 365

Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
 370 375 380

Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp
 385 390 395 400

Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
 405 410 415

Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr
 420 425 430

Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
 435 440 445

Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
 450 455 460

Asp Trp Tyr Asn Asn Ser Asp Trp Tyr Asn Asn
 465 470 475

<210> 5

<211> 1299

<212> DNA

<213> Bacillus thuringiensis

<400> 5

atgggtctga ttacacacaat caagctgaac tctaacaaga agtatggtcc tggcgatatg 60

actaacggga accagttcat catatccaag caagaatggg ccacgattgg cgcatacatt 120

cagactggac tcggcttacc agtgaatgag caacagctga gaaccacgt taaccttagt 180

caagacatca gcataccatc tgacttttct caactctacg atgtgtattg ttctgacaag 240

actagtgcag aatggtggaa caagaatctc tatcctttga tcatcaagtc tgccaatgac 300
 attgcttcat atggtttcaa agttgctggt gatccttoga tcaagaaaga tggttacttc 360
 aagaagcttc aagatgaact cgacaacatt gttgacaaca actccgacga cgatgcgata 420
 gccaaagcca tcaaggactt caaagcaaga tgtggcattc tcatcaagga agccaagcag 480
 tatgaagaag ctgccaagaa cattgtaaca tcattggatc agttttctcca tggagaccag 540
 aagaagctcg aggggtgtcat caacattcag aaacgtctga aagaggttca aacagctctg 600
 aatcaagccc atggggaatc cagtccagct cacaagagac ttcttgagaa agtgaagaac 660
 ttgaagacca cacttgagag gaccatcaaa gctgaacaag acttgagaa gaaagtagag 720
 tacagctttc tacttgacc cttgttaggc tttgttgtct acgagattct tgagaacact 780
 gctgttcaac acatcaagaa tcaaatcgat gagatcaaga aacagttgga ttctgcgcaa 840
 catgacttgg atcgcgatgt gaagatcatt ggaatgctca acagcatcaa cactgacatt 900
 gacaacttgt atagtcaagg acaagaagca atcaaagtct ttcagaagct acaagggata 960
 tggggcacta ttggagctca gatagagaat cttcgacca cgtcccttca agaagtccaa 1020
 gactctgatg atgctgatga gatacagatt gaacttgagg acgcatctga tgcattggtta 1080
 gttgtggctc aagaagctcg tgacttcaca ctgaatgctt actcaaccaa cagtcgacag 1140
 aatctcccga tcaatgtgat ctcagattca tgcaattgct ccaccaccaa catgacatcc 1200
 aatcagtaca gcaatccaac aaccaacatg actagcaatc agtacatgat tagccatgag 1260
 tataaccagct tgcccaacaa cttcatgttg tcaaggtag 1299

<210> 6
 <211> 432
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 6

Met Gly Leu Ile His Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly
 1 5 10 15

Pro Gly Asp Met Thr Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu
 20 25 30

Trp Ala Thr Ile Gly Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val
 35 40 45

Asn Glu Gln Gln Leu Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser
50 55 60

Ile Pro Ser Asp Phe Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys
65 70 75 80

Thr Ser Ala Glu Trp Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys
85 90 95

Ser Ala Asn Asp Ile Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro
100 105 110

Ser Ile Lys Lys Asp Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp
115 120 125

Asn Ile Val Asp Asn Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile
130 135 140

Lys Asp Phe Lys Ala Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln
145 150 155 160

Tyr Glu Glu Ala Ala Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu
165 170 175

His Gly Asp Gln Lys Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg
180 185 190

Leu Lys Glu Val Gln Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser
195 200 205

Pro Ala His Lys Glu Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr
210 215 220

Leu Glu Arg Thr Ile Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu
225 230 235 240

Tyr Ser Phe Leu Leu Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile
245 250 255

Leu Glu Asn Thr Ala Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile
260 265 270

Lys Lys Gln Leu Asp Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys
 275 280 285

Ile Ile Gly Met Leu Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr
 290 295 300

Ser Gln Gly Gln Glu Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile
 305 310 315 320

Trp Ala Thr Ile Gly Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu
 325 330 335

Gln Glu Val Gln Asp Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu
 340 345 350

Glu Asp Ala Ser Asp Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp
 355 360 365

Phe Thr Leu Asn Ala Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile
 370 375 380

Asn Val Ile Ser Asp Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser
 385 390 395 400

Asn Gln Tyr Ser Asn Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met
 405 410 415

Ile Ser His Glu Tyr Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg
 420 425 430

<210> 7

<211> 1140

<212> DNA

<213> Bacillus thuringiensis

<400> 7

atgggtctga ttcacacaat caagctgaac tctaacaaga agtatgggtcc tggcgatatg 60

actaacggga accagttcat catatccaag caagaatggg ccacgattgg cgcatacatt 120

cagactggac tcggcttacc agtgaatgag caacagctga gaaccacgt taaccttagt 180

caagacatca gcataccatc tgacttttct caactctacg atgtgtattg ttctgacaag 240

actagtgcag aatgggtggaa caagaatctc tatcctttga tcatcaagtc tgccaatgac 300

attgcttcat atgggttcaa agttgctggg gatccttcga tcaagaaaga tggttacttc 360

```

aagaagcttc aagatgaact cgacaacatt gttgacaaca actccgacga cgatgcgata 420
gccaaagcca tcaaggactt caaagcaaga tgtggcattc tcatcaagga agccaagcag 480
tatgaagaag ctgccaagaa cattgtaaca tcattggatc agtttctcca tggagaccag 540
aagaagctcg aggggtgcat caacattcag aaacgtctga aagaggttca aacagctctg 600
aatcaagccc atggggaatc cagtccagct cacaagagc ttcttgagaa agtgaagaac 660
ttgaagacca cacttgagag gaccatcaaa gctgaacaag acttgagaa gaaagtagag 720
tacagctttc tacttgagacc cttgttaggc tttgttgtct acgagattct tgagaacact 780
gctgttcaac acatcaagaa tcaaatcgat gagatcaaga aacagttgga ttctgcgcaa 840
catgacttgg atcgcgatgt gaagatcatt ggaatgctca acagcatcaa cactgacatt 900
gacaacttgt atagtcaagg acaagaagca atcaaagtct ttcagaagct acaagggata 960
tgggccacta ttggagctca gatagagaat cttcgcacca cgtcccttca agaagtccaa 1020
gactctgatg atgctgatga gatacagatt gaacttgagg acgcatctga tgcattggta 1080
gttgtggctc aagaagctcg tgacttcaca ctgaatgcct actcaaccaa cagtcgatag 1140

```

<210> 8

<211> 380

<212> PRT

<213> *Bacillus thuringiensis*

<400> 8

```

Met Gly Leu Ile His Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly
1           5           10          15

```

```

Pro Gly Asp Met Thr Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu
          20          25          30

```

```

Trp Ala Thr Ile Gly Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val
          35          40          45

```

```

Asn Glu Gln Gln Leu Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser
          50          55          60

```

```

Ile Pro Ser Asp Phe Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys
        65          70          75          80

```

```

Thr Ser Ala Glu Trp Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys
          85          90          95

```

Ser Ala Asn Asp Ile Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro
 100 105 110

Ser Ile Lys Lys Asp Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp
 115 120 125

Asn Ile Val Asp Asn Asn Ser Asp Asp Ala Ile Ala Lys Ala Ile
 130 135 140

Lys Asp Phe Lys Ala Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln
 145 150 155 160

Tyr Glu Glu Ala Ala Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu
 165 170 175

His Gly Asp Gln Lys Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg
 180 185 190

Leu Lys Glu Val Gln Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser
 195 200 205

Pro Ala His Lys Glu Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr
 210 215 220

Leu Glu Arg Thr Ile Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu
 225 230 235 240

Tyr Ser Phe Leu Leu Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile
 245 250 255

Leu Glu Asn Thr Ala Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile
 260 265 270

Lys Lys Gln Leu Asp Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys
 275 280 285

Ile Ile Gly Met Leu Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr
 290 295 300

Ser Gln Gly Gln Glu Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile
 305 310 315 320

S:\SHARE\Sequences\MA-702D2.ST25.txt/DNB/ehm

agtgttataa gtcttaatat cggcaatctt cgagaaacat ctttaaaaga gatagaagaa 1080
 gaaaatgatg acgatgcact gtatattgag cttggtgatg ccgctggtca atggaaagag 1140
 atagccgagg aggcacaatc ctttgtacta aatgcttata ctcct 1185

<210> 10
 <211> 208
 <212> PRT
 <213> Bacillus thuringiensis

<400> 10

Met Ile Leu Gly Asn Gly Lys Thr Leu Pro Lys His Ile Arg Leu Ala
 1 5 10 15

His Ile Phe Ala Thr Gln Asn Ser Ser Ala Lys Lys Asp Asn Pro Leu
 20 25 30

Gly Pro Glu Gly Met Val Thr Lys Asp Gly Phe Ile Ile Ser Lys Glu
 35 40 45

Glu Trp Ala Phe Val Gln Ala Tyr Val Thr Thr Gly Thr Gly Leu Pro
 50 55 60

Ile Asn Asp Asp Glu Met Arg Arg His Val Gly Leu Pro Ser Arg Ile
 65 70 75 80

Gln Ile Pro Asp Asp Phe Asn Gln Leu Tyr Lys Val Tyr Asn Glu Asp
 85 90 95

Lys His Leu Cys Ser Trp Trp Asn Gly Phe Leu Phe Pro Leu Val Leu
 100 105 110

Lys Thr Ala Asn Asp Ile Ser Ala Tyr Gly Phe Lys Cys Ala Gly Lys
 115 120 125

Gly Ala Thr Lys Gly Tyr Tyr Glu Val Met Gln Asp Asp Val Glu Asn
 130 135 140

Ile Ser Asp Asn Gly Tyr Asp Lys Val Ala Gln Glu Lys Ala His Lys
 145 150 155 160

Asp Leu Gln Ala Arg Cys Lys Ile Leu Ile Lys Glu Ala Asp Gln Tyr
 165 170 175

Lys Ala Ala Ala Asp Asp Val Ser Lys His Leu Asn Thr Phe Leu Lys
180 185 190

Gly Gly Gln Asp Ser Asp Gly Asn Asp Val Ile Gly Val Glu Ala Val
195 200 205

MA-702D2
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210